

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 7, 2002, 15:11:37 ; Search time 0.29 Seconds

(without alignments)  
4.216 Million cell updates/sec

Title: us-09-783-320-6

Sequence: 1 MKNLVKLIISGSPVSLHY.....YAKILHVMADGAYQEDNDE 1007

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1214 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database: us-09-783-320-4:\*

Pred. No: is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	5162	100.0	1214	1	us-09-783-320-4

#### ALIGNMENTS

RESULT 1  
us-09-783-320-4

Query Match 100.08; Score 5162; DB 1; Length 1214;  
Best Local Similarity 100.08; Pred. No. 0;  
Matches 1007; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKNLVKLIISGSPVSLHYSDLRSLVSLQFLKRNDRDRPSVNSILEKGFIAKRIEKL	60
DB	208	MKNLVKLIISGSPVSLHYSDLRSLVSLQFLKRNDRDRPSVNSILEKGFIAKRIEKL	267
QY	61	POLIAEEFCLTFSKFGSOPIPAKRPASGONSISVPAOKITPKPAKYGIPLAYKKYGD	120
DB	268	POLIAEEFCLTFSKFGSOPIPAKRPASGONSISVPAOKITPKPAKYGIPLAYKKYGD	327
QY	121	KLHEKKPLQKHQAHOTPEKRVNTGEERKISEEAKRRRLFEIEKKKKOQIISLMA	180
DB	328	KLHEKKPLQKHQAHOTPEKRVNTGEERKISEEAKRRRLFEIEKKKKOQIISLMA	387
QY	181	EOMKROEKERLERINRAREOGNRNVLASGSGEVKAPFLGSGGTAPSSFSRGOYEHY	240
DB	388	EOMKROEKERLERINRAREOGNRNVLASGSGEVKAPFLGSGGTAPSSFSRGOYEHY	447
QY	241	ALFDMOQOQRAEDNNAKKKRELYGRLGIPROKGLAVERAKOYEFLQRRKREAMONK	300
DB	448	ALFDMOQOQRAEDNNAKKKRELYGRLGIPROKGLAVERAKOYEFLQRRKREAMONK	507

QY	301	EGHNVYLARLQIRLQNFNEROQIKAKLGERKEANHSOGSGSEADMRKKIESLKAH	360
DB	508	EGHNVYLARLQIRLQNFNEROQIKAKLGERKEANHSOGSGSEADMRKKIESLKAH	567
QY	361	ANARAAYLKEOLEERKKBAVERERKKVWEHLLAKGVKSSDVSPPLQGHETGSGSPSKO	420
DB	568	ANARAAYLKEOLEERKKBAVERERKKVWEHLLAKGVKSSDVSPPLQGHETGSGSPSKO	627
QY	421	SVISVTSALKEGVDSLTDRFRETSEEMOKTNNALSSKREILRLRLNENKKAODEKGM	480
DB	628	SVISVTSALKEGVDSLTDRFRETSEEMOKTNNALSSKREILRLRLNENKKAODEKGM	687
QY	481	LSDFPEINWHEDAKHEKEKSVSSDRKKWEAGOLVPIDELDTLDTFSFSTERHTYGEV	540
DB	688	LSDFPEINWHEDAKHEKEKSVSSDRKKWEAGOLVPIDELDTLDTFSFSTERHTYGEV	747
QY	541	KLGPNGSPRRAMGKSPDTSVLKILGEAELOLDTLELLENTTISEISPEGEKYPPLITGE	600
DB	748	KLGPNGSPRRAMGKSPDTSVLKILGEAELOLDTLELLENTTISEISPEGEKYPPLITGE	807
QY	601	KVOCISHEINSAIVDSPEYETKSPFESEASPOWSILKLEGNLEPPDLLETLIOEPGCTN	660
DB	808	KVOCISHEINSAIVDSPEYETKSPFESEASPOWSILKLEGNLEPPDLLETLIOEPGCTN	867
QY	661	DESLPCTITDVMISEEKETKETQSDRITIOENESVEDGVSTVDLSDIHEPGTND	720
DB	868	DESLPCTITDVMISEEKETKETQSDRITIOENESVEDGVSTVDLSDIHEPGTND	927
QY	721	HSKCDVDKSVQEPFPHKVVHSEHLNLPVOVOSVOCSPSEFAFRSHSLPPKNNKNSL	780
DB	928	HSKCDVDKSVQEPFPHKVVHSEHLNLPVOVOSVOCSPSEFAFRSHSLPPKNNKNSL	987
QY	781	LIGLSTGLFDANNPMLRTCSLPDLSKLFTLMDVPTVGDVRODNEIDEIKDENIKEG	840
DB	988	LIGLSTGLFDANNPMLRTCSLPDLSKLFTLMDVPTVGDVRODNEIDEIKDENIKEG	1047
QY	841	SDSEDIIVEETDLOEOLOASMEOLLEOPEGEYSSEESVILKNSVPEPTANGTDAED	900
DB	1048	SDSEDIIVEETDLOEOLOASMEOLLEOPEGEYSSEESVILKNSVPEPTANGTDAED	1107
QY	901	DNPSSSEALNEEMHSDNSGCEJASBCECDSVNHLLELRLHLEQENGFEFFVEYETIK	960
DB	1108	DNPSSSEALNEEMHSDNSGCEJASBCECDSVNHLLELRLHLEQENGFEFFVEYETIK	1167
QY	961	IHEDEDNEIECKIVONITLGNHOLYAKIILHLYVADGAYQEDNDE 1007	
DB	1168	IHEDEDNEIECKIVONITLGNHOLYAKIILHLYVADGAYQEDNDE 1214	

Search completed: May 7, 2002, 15:11:39  
Job time: 2 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2002, 15:09:25 ; Search time 5.77 Seconds  
(without alignments)  
3.821 Million cell updates/sec

Title: us-09-783-320-5

Perfect score: 3024  
Sequence: 1 atgaaaaacctgtaactgaa.....aagaataatgataataa 3024

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 3645 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : us-09-783-320-3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3024	100.0	3645	1	us-09-783-320-3	
2	28.8	1.0	3645	1	us-09-783-320-3	

## ALIGNMENTS

RESULT 1  
us-09-783-320-3

Query Match 100.0%; Score 3024; DB 1; Length 3645;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3024; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	atgaaaaacctgtaactgaaataatctgttccacctggtcttgcattat	60
DB	622	atgaaaaacctgtaactgaaataatctgttccacctggtcttgcattat	681
QY	61	tccatgatactccgcaggttgggtctcagttatataaagaatccctaggatagaca	120
DB	682	tccatgatactccgcaggttgggtctcagttatataaagaatccctaggatagaca	741
QY	121	tcaagtaactccatattggaagaagtttatagccaacgcatlgaagaattctctct	180
DB	742	tcaagtaactccatattggaagaagtttatagccaacgcatlgaagaattctctct	801
QY	181	cctcagctatttcagagaagatttgcataaacaatttcgaagtttgatcacagcct	240
DB	802	cctcagctatttcagagaagatttgcataaacaatttcgaagtttgatcacagcct	861
QY	241	ataccgcttaaaagaccagcttcagagacaacatcgtattcgttatcgctcagaaa	300

DB	862	ataccgcttaaaagaccagcttcagagacaacatcgtattcgttatcgctcagaaa	921
QY	301	attacaaagcttcgcgttaataatgaaatccctttagcatataagaataatggagataa	360
DB	922	attacaaagcttcgcgttaataatgaaatccctttagcatataagaataatggagataa	981
QY	361	aaattacagaaaagaagaccatgcgcaaaaataaagaagccatcaactccgagaag	420
DB	982	aaattacagaaaagaagaccatgcgcaaaaataaagaagccatcaactccgagaag	1041
QY	421	agagtgaatactcggagagaagaaggaataatctcgaagaagcagcagaagaagaag	480
DB	1042	agagtgaatactcggagagaagaaggaataatctcgaagaagcagcagaagaagaag	1101
QY	481	ctggaatttatgaaaaagaagaacaaagatcagattatatttaattaaagct	540
DB	1102	ctggaatttatgaaaaagaagaacaaagatcagattatatttaattaaagct	1161
QY	541	gaacaatgaaaagcgaagaagaaggtttggaagaataataggccaggaaca	600
DB	1162	gaacaatgaaaagcgaagaagaaggtttggaagaataataggccaggaaca	1221
QY	601	gagtgagaatgtgctaaagtgtgtggaagtgtgaatgaaggtcctttctggc	660
DB	1222	gagtgagaatgtgctaaagtgtgtggaagtgtgaatgaaggtcctttctggc	1281
QY	661	agtggaggaactaagctccatcatctttcttcgagagacagttgacattacat	720
DB	1282	agtggaggaactaagctccatcatctttcttcgagagacagttgacattacat	1341
QY	721	gccattttgacaaatgacgacacaaagcgaagaataatgaagtaatgaaaga	780
DB	1342	gccattttgacaaatgacgacacaaagcgaagaataatgaagtaatgaaaga	1401
QY	781	gaaatatagtgtcgaaggtcttccagaagaagcagcagctgtatagaagaagct	840
DB	1402	gaaatatagtgtcgaaggtcttccagaagaagcagcagctgtatagaagaagct	1461
QY	841	aaacaagtagaagatctcctgcagcaaaacggaagctatgcgaataaagctcgacc	900
DB	1462	aaacaagtagaagatctcctgcagcaaaacggaagctatgcgaataaagctcgacc	1521
QY	901	gaagacataatgtttatctcgaagaactgagcaaaataagactacagaatttcaatgag	960
DB	1522	gaagacataatgtttatctcgaagaactgagcaaaataagactacagaatttcaatgag	1581
QY	961	cgccacaagattaagccaaactcgtgtgtgaagaagaagcctaacttctgaagga	1020
DB	1582	cgccacaagattaagccaaactcgtgtgtgaagaagaagcctaacttctgaagga	1641
QY	1021	caagaagaagtgaaagagctgacatgaaagcgaaaaaataatcgaatcgaagcccat	1080
DB	1642	caagaagaagtgaaagagctgacatgaaagcgaaaaaataatcgaatcgaagcccat	1701
QY	1081	gcaaatgacgtgtgtgttactcaaaaagaacaactgaaagaaagaagaagagcttat	1140
DB	1702	gcaaatgacgtgtgtgttactcaaaaagaacaactgaaagaaagaagaagagcttat	1761
QY	1141	gagagagaaaaaaagttgtggaagaagcatttgggtgctaaaggaagtttaagttcgtat	1200
DB	1762	gagagagaaaaaaagttgtggaagaagcatttgggtgctaaaggaagtttaagttcgtat	1821
QY	1201	gtttctcaccttttggagaagcagtaaacaggtgtgtctccatcaaacgacaagatgaga	1260
DB	1822	gtttctcaccttttggagaagcagtaaacaggtgtgtctccatcaaacgacaagatgaga	1881
QY	1261	tctgtatttctgtaactcagcttgaagaaggttggcgtggaacagtaatttaacgat	1320
DB	1882	tctgtatttctgtaactcagcttgaagaaggttggcgtggaacagtaatttaacgat	1941
QY	1321	accgggaactcagaagaagatgacaaagacaaacaaatctatccaagttaacggagaa	1380
DB	1942	accgggaactcagaagaagatgacaaagacaaacaaatctatccaagttaacggagaa	2001

QY	1381	aacttcgcgagatctaaatctgaaatcttaagctccaaagatctgaataaggaatgcagat	1440
Db	2002	atacttcgcgcagatctaaatctgaaatcttaagctccaaagatctgaataaggaatgcagat	2061
QY	1441	ctctctgatactcttgagataaagtctcagatgagtcgaaagagcatgaaaaagaanaa	1500
Db	2062	ctctctgatactcttgagataaagtctcagatgagtcgaaagagcatgaaaaagaanaa	2121
QY	1501	tcagtttcatactgcgcgaagaagtgggaagcgagagtcgaactgcatctccctgagat	1560
Db	2122	tcagtttcatactgcgcgaagaagtgggaagcgagagtcgaactgcatctccctgagat	2181
QY	1561	gaattacaactagaatcactcctctccacacgcgaagacatacagtggggaagttat	1620
Db	2182	gaattacaactagaatcactcctctccacacgcgaagacatacagtggggaagttat	2241
QY	1621	aaattggttcctatagatctccaaagaagcctgggggaagaagtcgcaagatctcgt	1680
Db	2242	aaattggttcctatagatctccaaagaagcctgggggaagaagtcgcaagatctcgt	2301
QY	1681	ctaaagatctctggagaagctgtaactacaactccagacagaactatagaataacact	1740
Db	2302	ctaaagatctctggagaagctgtaactacaactccagacagaactatagaataacact	2361
QY	1741	attagaagtggagaattctcccggaagggaagaatgacaaaccttaattactggaanaa	1800
Db	2362	attagaagtggagaattctcccggaagggaagaatgacaaaccttaattactggaanaa	2421
QY	1801	aaagtacaatgtaattccacatagaataaaccgatcgactgttgatctccgttgag	1860
Db	2422	aaagtacaatgtaattccacatagaataaaccgatcgactgttgatctccgttgag	2481
QY	1861	acaaaaagccccagatctcagtgaggcatctccacagaatgcatctgaaactgggaagaaat	1920
Db	2482	acaaaaagccccagatctcagtgaggcatctccacagaatgcatctgaaactgggaagaaat	2541
QY	1921	ttagaagaacctgatagtattggaaaaagaataattctacaagaagccaaatggaaacaaa	1980
Db	2542	ttagaagaacctgatagtattggaaaaagaataattctacaagaagccaaatggaaacaaa	2601
QY	1981	gattgagacttgacatgcatctactgatagttgatttagtgagagaaaaagaacaaag	2040
Db	2602	gattgagacttgacatgcatctactgatagttgatttagtgagagaaaaagaacaaag	2661
QY	2041	gaacatcagctcggcagatagatctacacatctcagaagaatgaagtctctgaaagtgc	2100
Db	2662	gaacatcagctcggcagatagatctacacatctcagaagaatgaagtctctgaaagtgc	2721
QY	2101	tcgagatcgtggaaccaacttaattgacatctacataagagcctggaaaccaattgctcag	2160
Db	2722	tcgagatcgtggaaccaacttaattgacatctacataagagcctggaaaccaattgctcag	2781
QY	2161	caactcaaatgtagatgaataagtcctgtgcaacccggaaccaattctccaagtgtgt	2220
Db	2782	caactcaaatgtagatgaataagtcctgtgcaacccggaaccaattctccaagtgtgt	2841
QY	2221	catctgaaacctgaaacttaagtccctcaagtctcaatcagttcagtttccacaagaaga	2280
Db	2842	catctgaaacctgaaacttaagtccctcaagtctcaatcagttcagtttccacaagaaga	2901
QY	2281	tcctctgcaattcgatctcactcgcattctaccccaaaaaataaaaaagaattcctgt	2340
Db	2902	tcctctgcaattcgatctcactcgcattctaccccaaaaaataaaaaagaattcctgt	2961
QY	2341	ccgattggaactctcaactgtcgtttgttagtgcaaaacccaaagaatgttaagaatgt	2400
Db	2962	ccgattggaactctcaactgtcgtttgttagtgcaaaacccaaagaatgttaagaatgt	3021
QY	2401	tcacttcagatctctcaaaagctgtctcagaaaccttaatgtagtctccacccgttagagat	2460
Db	3022	tcacttcagatctctcaaaagctgtctcagaaaccttaatgtagtctccacccgttagagat	3081

OY	2461	gtctgcgaagacaactcttgaanaataagatgtgaatataagaatgaaacaacttaagaagaagact	2520
Db	3082	gtctgcgaagacaactcttgaanaataagatgtgaatataagaatgaaacaacttaagaagaagact	3141
OY	2521	tctgattctggaagaccttcttcttgaagaagaactgcagacagatttaaaagctgcagagcc	2580
Db	3142	tctgattctggaagaccttcttcttgaagaagaactgcagacagatttaaaagctgcagagcc	3201
OY	2581	tctgattggaacatttacttactttagggaaacaacctgtrtgaagaataacatgtaaaaaaagaagtca	2640
Db	3202	tctgattggaacatttacttactttagggaaacaacctgtrtgaagaataacatgtaaaaaaagaagtca	3261
OY	2641	gtcttgaagaanaaagrbatgttgagtgagccaactgtrgaatgaatggagacagatctggcagatgaagt	2700
Db	3262	gtcttgaagaanaaagrbatgttgagtgagccaactgtrgaatgaatggagacagatctggcagatgaagt	3321
OY	2701	ggacattcccaagtatgtagaagaagtgcctctgaaacgaagaatgtgcactcaagataacagtatggt	2760
Db	3322	ggacattcccaagtatgtagaagaagtgcctctgaaacgaagaatgtgcactcaagataacagtatggt	3381
OY	2761	ggaatttgtctagtgtatgtatgtatgtagtcgatgtgtctcttaaccatttaagaagaactgagaact	2820
Db	3382	ggaatttgtctagtgtatgtatgtatgtagtcgatgtgtgtctcttaaccatttaagaagaactgagaact	3441
OY	2821	catctggaacagagaagaatgagcttctgaaaaaattcctcttgaggtctatagagaanaataaagct	2880
Db	3442	catctggaacagagaagaatgagcttctgaaaaaattcctcttgaggtctatagagaanaataaagct	3501
OY	2881	attcatggaagtatgaagtatgaanaatatggaatattgtgttccaanaataagttccaanaatatcttg	2940
Db	3502	attcatggaagtatgaagtatgaanaatatggaatattgtgttccaanaataagttccaanaatatcttg	3561
OY	2941	ggaatatggaacatcacaatctcttatctccaagattctcatttatgtaactgagcagatgagacc	3000
Db	3562	ggaatatggaacatcacaatctcttatctccaagattctcatttatgtaactgagcagatgagacc	3621
OY	3001	taccagaagaagataatgatgaataa 3024	
Db	3622	taccagaagaagataatgatgaataa 3645	

RESULT 2  
us-09-783-320-3/c

Query Match	1.0%	Score	28.8	DB	1	length	3645
Best Local Similarity	53.6%	Pred No.	0				
Matches	60	Conservative	0	Mismatches	52	Indels	0
				Gaps			0

OY 2869 aaaaataagagcattcaatgaagtgaggaatgaagaatcttgcataaagt 2928  
 Db 3601 ATGGAAGATCTTGCGATAAAGTCTGAGCTTCATTTCCCAAAATTTTGAACATA 3542  
 OY 2929 caaatattctggaaatgaacatcagcatcttatagcgaagtctcatt 2980  
 Db 3541 TTGAACCAATTTCCAAATTTTCACTCTTCATCTTCATCATTAATAGCCCTATATT 3490

Search completed: May 7, 2002, 15:09:42  
Job time: 17 sec